

## REPEAT-FREE PROBES FOR MOLECULAR CYTOGENETICS

### ABSTRACT OF THE DISCLOSURE

The present invention provides a rapid, efficient, and automated method for identifying unique sequences within the genome. This invention involves the identification of repeat sequence-free subregions within a genomic region of interest as well as the determination of which of those repeat sequence-free subregions are truly unique within the genome. Once the truly unique subregions are identified, primer sequences are generated that are suitable for the amplification of sequences, *e.g.*, for use as probes or array targets, within the unique subregions.

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